RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/511,833_
Source: _PCT/JP_
Date Processed by STIC: _10/29/04_

ENTERED

RAW SEQUENCE LISTING   DATE: 10/29/2004
PATENT APPLICATION: US/10/511,832 TIME: 11:33:33

Input Set : A:\ISIS0048-100.SEQ.txt
Output Set: N:\CRF4\10292004\J511832.raw

```
   4 <110> APPLICANT: Susan M. Freier
   6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF HYDROXYSTEROID
   7       11-BETA DEHYDROGENASE 1 EXPRESSION
  10 <130> FILE REFERENCE: RTS-0428
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/511,832
C--> 12 <141> CURRENT FILING DATE: 2004-10-19
  12 <160> NUMBER OF SEQ ID NOS: 122
  14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  16 <210> SEQ ID NO: 1
  17 <211> LENGTH: 20
  18 <212> TYPE: DNA
  19 <213> ORGANISM: Artificial Sequence
  21 <220> FEATURE:
  22 <223> OTHER INFORMATION: Antisense Oligonucleotide
  24 <400> SEQUENCE: 1
  25 tccgtcatcg ctcctcaggg                                        20
  27 <210> SEQ ID NO: 2
  28 <211> LENGTH: 20
  29 <212> TYPE: DNA
  30 <213> ORGANISM: Artificial Sequence
  32 <220> FEATURE:
  33 <223> OTHER INFORMATION: Antisense Oligonucleotide
  35 <400> SEQUENCE: 2
  36 atgcattctg cccccaagga                                        20
  38 <210> SEQ ID NO: 3
  39 <211> LENGTH: 1375
  40 <212> TYPE: DNA
  41 <213> ORGANISM: Homo sapiens
  43 <220> FEATURE:
  44 <221> NAME/KEY: CDS
  45 <222> LOCATION: (95)...(973)
  47 <400> SEQUENCE: 3
  48 attcagaggc tgctgcctgc ttaggaggtt gtagaaagct ctgtaggttc tctctgtgtg 60
  49 tcctacagga gtcttcaggc cagctccctg tcgg atg gct ttt atg aaa aaa tat 115
  50                                     Met Ala Phe Met Lys Lys Tyr
  51                                      1               5
  53 ctc ctc ccc att ctg ggg ctc ttc atg gcc tac tac tac tat tct gca 163
  54 Leu Leu Pro Ile Leu Gly Leu Phe Met Ala Tyr Tyr Tyr Tyr Ser Ala
  55          10              15                  20
  57 aac gag gaa ttc aga cca gag atg ctc caa gga aag aaa gtg att gtc 211
  58 Asn Glu Glu Phe Arg Pro Glu Met Leu Gln Gly Lys Lys Val Ile Val
  59      25              30              35
  61 aca ggg gcc agc aaa ggg atc gga aga gag atg gct tat cat ctg gcg 259
```

```
62 Thr Gly Ala Ser Lys Gly Ile Gly Arg Glu Met Ala Tyr His Leu Ala
63    40                  45                  50                  55
65 aag atg gga gcc cat gtg gtg gtg aca gcg agg tca aaa gaa act cta   307
66 Lys Met Gly Ala His Val Val Val Thr Ala Arg Ser Lys Glu Thr Leu
67                  60                  65                  70
69 cag aag gtg gta tcc cac tgc ctg gag ctt gga gca gcc tca gca cac   355
70 Gln Lys Val Val Ser His Cys Leu Glu Leu Gly Ala Ala Ser Ala His
71                  75                  80                  85
73 tac att gct ggc acc atg gaa gac atg acc ttc gca gag caa ttt gtt   403
74 Tyr Ile Ala Gly Thr Met Glu Asp Met Thr Phe Ala Glu Gln Phe Val
75                  90                  95                  100
77 gcc caa gca gga aag ctc atg gga gga cta gac atg ctc att ctc aac   451
78 Ala Gln Ala Gly Lys Leu Met Gly Gly Leu Asp Met Leu Ile Leu Asn
79     105                 110                 115
81 cac atc acc aac act tct ttg aat ctt ttt cat gat gat att cac cat   499
82 His Ile Thr Asn Thr Ser Leu Asn Leu Phe His Asp Asp Ile His His
83 120                 125.                130                 135
85 gtg cgc aaa agc atg gaa gtc aac ttc ctc agt tac gtg gtc ctg act   547
86 Val Arg Lys Ser Met Glu Val Asn Phe Leu Ser Tyr Val Val Leu Thr
87                 140                 145                 150
89 gta gct gcc ttg ccc atg ctg aag cag agc aat gga agc att gtt gtc   595
90 Val Ala Ala Leu Pro Met Leu Lys Gln Ser Asn Gly Ser Ile Val Val
91             155                 160                 165
93 gtc tcc tct ctg gct ggg aaa gtg gct tat cca atg gtt gct gcc tat   643
94 Val Ser Ser Leu Ala Gly Lys Val Ala Tyr Pro Met Val Ala Ala Tyr
95         170                 175                 180
97 tct gca agc aag ttt gct ttg gat ggg ttc ttc tcc tcc atc aga aag   691
98 Ser Ala Ser Lys Phe Ala Leu Asp Gly Phe Phe Ser Ser Ile Arg Lys
99     185                 190                 195
101 gaa tat tca gtg tcc agg gtc aat gta tca atc act ctc tgt gtt ctt  739
102 Glu Tyr Ser Val Ser Arg Val Asn Val Ser Ile Thr Leu Cys Val Leu
103 200                 205                 210                 215
105 ggc ctc ata gac aca gaa aca gcc atg aag gca gtt tct ggg ata gtc  787
106 Gly Leu Ile Asp Thr Glu Thr Ala Met Lys Ala Val Ser Gly Ile Val
107                 220                 225                 230
109 cat atg caa gca gct cca aag gag gaa tgt gcc ctg gag atc atc aaa  835
110 His Met Gln Ala Ala Pro Lys Glu Glu Cys Ala Leu Glu Ile Ile Lys
111             235                 240                 245
113 ggg gga gct ctg cgc caa gaa gaa gtg tat tat gac agc tca ctc tgg  883
114 Gly Gly Ala Leu Arg Gln Glu Glu Val Tyr Tyr Asp Ser Ser Leu Trp
115         250                 255                 260
117 acc act ctt ctg atc aga aat cca tgc agg aag atc ctg gaa ttt ctc  931
118 Thr Thr Leu Leu Ile Arg Asn Pro Cys Arg Lys Ile Leu Glu Phe Leu
119     265                 270                 275
121 tac tca acg agc tat aat atg gac aga ttc ata aac aag tag          973
122 Tyr Ser Thr Ser Tyr Asn Met Asp Arg Phe Ile Asn Lys  *
123 280                 285                 290
125 gaactccctg agggctgggc atgctgaggg attttgggac tgttctgtct catgtttatc 1033
126 tgagctctta tctatgaaga catcttccca gagtgtcccc agagacatgc aagtcatggg 1093
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127 tcacacctga caaatggaag gagttcctct aacatttgca aaatggaaat gtaataataa 1153
128 tgaatgtcat gcaccgctgc agccagcagt tgtaaaattg ttagtaaaca taggtataat 1213
129 taccagatag ttatattaaa tttatatctt atatataata atatgtgatg attaatacaa 1273
130 tattaattat aataaaggtc acataaactt tataaattca taactggtag ctataacttg 1333
131 agcttattca ggatggttct ttaaaccata aactgtacaa tg               1375
133 <210> SEQ ID NO: 4
134 <211> LENGTH: 24
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: PCR Primer
141 <400> SEQUENCE: 4
142 gtttctggga tagtccatat gcaa                                    24
144 <210> SEQ ID NO: 5
145 <211> LENGTH: 21
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: PCR Primer
152 <400> SEQUENCE: 5
153 agctcccccct ttgatgatct c                                      21
155 <210> SEQ ID NO: 6
156 <211> LENGTH: 25
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: PCR Probe
163 <400> SEQUENCE: 6
164 cagctccaaa ggaggaatgt gccct                                   25
166 <210> SEQ ID NO: 7
167 <211> LENGTH: 19
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: PCR Primer
175 <400> SEQUENCE: 7
176 gaaggtgaag gtcggagtc                                          19
178 <210> SEQ ID NO: 8
179 <211> LENGTH: 20
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: PCR Primer
187 <400> SEQUENCE: 8
188 gaagatggtg atgggatttc                                         20
190 <210> SEQ ID NO: 9
191 <211> LENGTH: 20
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
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```
195 <220> FEATURE:
196 <223> OTHER INFORMATION: PCR Probe
198 <400> SEQUENCE: 9
199 caagcttccc gttctcagcc                                        20
201 <210> SEQ ID NO: 10
202 <211> LENGTH: 1350
203 <212> TYPE: DNA
204 <213> ORGANISM: Mus musculus
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (128)...(1006)
210 <400> SEQUENCE: 10
211 ggatgagaca gaaggataga gaggaggaga gagagagaga gaagagaagc aaccagaaat 60
212 aggcagccaa taaaaaggag ccgcacttat ctgaagcctc aaggggcctg agccaggtcc 120
213 ctgtttg atg gca gtt atg aaa aat tac ctc ctc ccg atc ctg gtg ctc   169
214         Met Ala Val Met Lys Asn Tyr Leu Leu Pro Ile Leu Val Leu
215           1               5                  10
217 tcc ctg gcc tac tac tac tat tct aca aat gaa gag ttc aga cca gaa   217
218 Ser Leu Ala Tyr Tyr Tyr Tyr Ser Thr Asn Glu Glu Phe Arg Pro Glu
219  15               20                  25                  30
221 atg ctc cag gga aag aaa gtg att gtc act ggg gcc agc aaa ggg att   265
222 Met Leu Gln Gly Lys Lys Val Ile Val Thr Gly Ala Ser Lys Gly Ile
223                  35                  40                  45
225 gga aga gaa atg gca tat cat ctg tca aaa atg gga gcc cat gtg gta   313
226 Gly Arg Glu Met Ala Tyr His Leu Ser Lys Met Gly Ala His Val Val
227                  50                  55                  60
229 ttg act gcc agg tcg gag gaa ggt ctc cag aag gta gtg tct cgc tgc   361
230 Leu Thr Ala Arg Ser Glu Glu Gly Leu Gln Lys Val Val Ser Arg Cys
231                  65                  70                  75
233 ctt gaa ctc gga gca gcc tct gct cac tac att gct ggc act atg gaa   409
234 Leu Glu Leu Gly Ala Ala Ser Ala His Tyr Ile Ala Gly Thr Met Glu
235          80                  85                  90
237 gac atg aca ttt gcg gag caa ttt att gtc aag gcg gga aag ctc atg   457
238 Asp Met Thr Phe Ala Glu Gln Phe Ile Val Lys Ala Gly Lys Leu Met
239  95                 100                 105                 110
241 ggc gga ctg gac atg ctt att cta aac cac atc act cag acc tcg ctg   505
242 Gly Gly Leu Asp Met Leu Ile Leu Asn His Ile Thr Gln Thr Ser Leu
243                 115                 120                 125
245 tct ctc ttc cat gac gac atc cac tct gtg cga aga gtc atg gag gtc   553
246 Ser Leu Phe His Asp Asp Ile His Ser Val Arg Arg Val Met Glu Val
247                 130                 135                 140
249 aac ttc ctc agc tac gtg gtc atg agc aca gcc gcc ttg ccc atg ctg   601
250 Asn Phe Leu Ser Tyr Val Val Met Ser Thr Ala Ala Leu Pro Met Leu
251                 145                 150                 155
253 aag cag agc aat ggc agc att gcc gtc atc tcc tcc ttg gct ggg aaa   649
254 Lys Gln Ser Asn Gly Ser Ile Ala Val Ile Ser Ser Leu Ala Gly Lys
255          160                 165                 170
257 atg acc cag cct atg att gct ccc tac tct gca agc aag ttt gct ctg   697
258 Met Thr Gln Pro Met Ile Ala Pro Tyr Ser Ala Ser Lys Phe Ala Leu
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```
259 175                  180              185                 190
261 gat ggg ttc ttt tcc acc att aga aca gaa ctc tac ata acc aag gtc      745
262 Asp Gly Phe Phe Ser Thr Ile Arg Thr Glu Leu Tyr Ile Thr Lys Val
263                  195               200                 205
265 aac gtg tcc atc act ctc tgt gtc ctt ggc ctc ata gac aca gaa aca      793
266 Asn Val Ser Ile Thr Leu Cys Val Leu Gly Leu Ile Asp Thr Glu Thr
267                  210               215                 220
269 gct atg aag gaa atc tct ggg ata att gac gcc cta gct tct ccc aag      841
270 Ala Met Lys Glu Ile Ser Gly Ile Ile Asp Ala Leu Ala Ser Pro Lys
271          225               230               235
273 gag gag tgc gcc ctg gag atc atc aaa ggc aca gct cta cgc aaa agc      889
274 Glu Glu Cys Ala Leu Glu Ile Ile Lys Gly Thr Ala Leu Arg Lys Ser
275          240               245               250
277 gag gtg tac tat gac aaa ttg cct ttg act cca atc ctg ctt ggg aac      937
278 Glu Val Tyr Tyr Asp Lys Leu Pro Leu Thr Pro Ile Leu Leu Gly Asn
279 255                  260               265                 270
281 cca gga agg aag atc atg gaa ttt ttt tca tta cga tat tat aat aag      985
282 Pro Gly Arg Lys Ile Met Glu Phe Phe Ser Leu Arg Tyr Tyr Asn Lys
283                  275               280                 285
285 gac atg ttt gta agt aac tag gaactcctga gccctggtga gtggtcttag          1036
286 Asp Met Phe Val Ser Asn  *
287                  290
289 aacagtcctg cctcatactt cagtaagccc tacccacaaa agtatctttc cagagataca 1096
290 caaatttttgg ggtacacctc atcatgagaa attcttgcaa cacttgcaca gtgaaaatgt 1156
291 aattgtaata aatgtcacaa accactttgg gcctgcagtt gtgaacttga ttgtaactat 1216
292 ggatataaac acatagtggt tgtatcggct ttacctcaca ctgaatgaaa caatgataac 1276
293 taatgtaaca ttaaatataa taaaggtaat atcaacttcg taaatgcaaa aaaaaaaaaa 1336
294 aaaaaaaaaa aaaa                                                    1350
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296 <210> SEQ ID NO: 11
297 <211> LENGTH: 18
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: PCR Primer
304 <400> SEQUENCE: 11
305 ggcggactgg acatgctt   18
307 <210> SEQ ID NO: 12
308 <211> LENGTH: 22
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: PCR Primer
316 <400> SEQUENCE: 12
317 gagtggatgt cgtcatggaa ga   22
319 <210> SEQ ID NO: 13
320 <211> LENGTH: 31
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:

VERIFICATION SUMMARY   DATE: 10/29/2004
PATENT APPLICATION: US/10/511,832   TIME: 11:33:34

Input Set : A:\ISIS0048-100.SEQ.txt
Output Set: N:\CRF4\10292004\J511832.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date